

SCORE Search Results Details for Application 10796719 and Search Result 20070322_090632_us-10-796-719a-31.rag.

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:36:07 ; Search time 218 Seconds
              (without alignments)
              31.425 Million cell updates/sec
```

```
Title:      US-10-796-719A-31
Perfect score: 101
Sequence:   1 CCEYCCNPACTGCGY 14
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_200701:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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10796719 and Search Result
20070322 090635 us-10-796-719a-31.rup.

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:37:42 ; Search time 346 Seconds
              (without alignments)
              43.381 Million cell updates/sec
```

Title: US-10-796-719A-31
Perfect score: 101
Sequence: 1 CCEYCCNPACTGCGY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      UniProt_8.4:*
1:  uniprot_sprot:*
2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	93	92.1	61	2	Q6VEG7_ECOLI	Q6veg7 escherichia
2	93	92.1	61	2	Q6VEG8_ECOLI	Q6veg8 escherichia
3	93	92.1	72	1	HST2_ECOLI	Q47185 escherichia

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:47:23 ; Search time 51 Seconds
              (without alignments)
              24.028 Million cell updates/sec
```

Title: US-10-796-719A-31
Perfect score: 101
Sequence: 1 CCEYCCNPACTGCGY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	% Query
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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:48:07 ; Search time 186 Seconds
              (without alignments)
              34.866 Million cell updates/sec
```

```
Title:      US-10-796-719A-31
Perfect score: 101
Sequence:   1 CCEYCCNPACTGCGY 14
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_AA_Main:*
1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Query Length	DB	ID	Description
		%				

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:49:03 ; Search time 90 Seconds
              (without alignments)
              31.666 Million cell updates/sec
```

```
Title:      US-10-796-719A-31
Perfect score: 101
Sequence:   1 CCEYCCNPACTGCY 14
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_AA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 17:56:43 ; Search time 218 Seconds
              (without alignments)
              38.159 Million cell updates/sec
```

Title: US-10-796-719A-14
Perfect score: 112
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

```
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      A_Geneseq_200701:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: March 23, 2007, 17:59:13 ; Search time 344 Seconds
(without alignments)
52.983 Million cell updates/sec

Title: US-10-796-719A-14
Perfect score: 112
Sequence: 1 IDCCEICCNPACFGCLN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	112	100.0	17	2 Q9R581_VIBCH	Q9r581 vibrio chol
2	112	100.0	18	2 Q9R580_VIBCH	Q9r580 vibrio chol
3	112	100.0	19	2 Q9R579_VIBCH	Q9r579 vibrio chol

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:02:53 ; Search time 39 Seconds
              (without alignments)
              41.941 Million cell updates/sec
```

Title: US-10-796-719A-14
Perfect score: 112
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      PIR_80:*
            1:  pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID		Description
1	112	100.0	17	2	A54534		heat-stable enterotoxin

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:09:29 ; Search time 52 Seconds
              (without alignments)
              28.616 Million cell updates/sec
```

Title: US-10-796-719A-14
Perfect score: 112
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:09:38 ; Search time 184 Seconds
              (without alignments)
              42.797 Million cell updates/sec
```

Title: US-10-796-719A-14
Perfect score: 112
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Published_Applications_AA_Main:*
1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
--------	-------	------------------	--------	----	----	-------------

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:10:53 ; Search time 89 Seconds
              (without alignments)
              38.883 Million cell updates/sec
```

Title: US-10-796-719A-14
Perfect score: 112
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Published_Applications_AA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

```
Run on:      March 26, 2007, 12:02:53 ; Search time 53 Seconds
              (without alignments)
              23.121 Million cell updates/sec
```

Title: US-10-796-719A-31
Perfect score: 101
Sequence: 1 CCEYCCNPACTGCGY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Issued_Patents_AA:*
1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: March 26, 2007, 12:03:06 ; Search time 185 Seconds
(without alignments)
35.054 Million cell updates/sec

Title: US-10-796-719A-31
Perfect score: 101
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%				
No.	Score	Match Length	DB	ID	Description	

SCORE Search Results Details for Application
10796719 and Search Result
20070326_091535_us-10-796-719a-31.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10796719 and Search Result 20070326_091535_us-10-796-719a-31.rapbn.

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OM protein - protein search, using sw model

```
Run on:      March 26, 2007, 12:04:21 ; Search time 89 Seconds
              (without alignments)
              32.021 Million cell updates/sec
```

Title: US-10-796-719A-31
Perfect score: 101
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Published_Applications_AA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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